

12/31/2001

(STIC stat

Serial Number: 10/005,216

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lien name at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,216

DATE: 12/31/2001

TIME: 18:43:02

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\12312001\J005216.raw

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4 <110> APPLICANT: Allen, Keith D.
5 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CALCIUM ION
6 CHANNEL (Trp6) GENE DISRUPTIONS
7
10 <130> FILE REFERENCE: R-881
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/005,216
C--> 12 <141> CURRENT FILING DATE: 2001-12-04
12 <150> PRIOR APPLICATION NUMBER: US 60/280,373
13 <151> PRIOR FILING DATE: 2001-03-29
15 <150> PRIOR APPLICATION NUMBER: US 60/255,227
16 <151> PRIOR FILING DATE: 2000-12-11
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3261
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
27 <400> SEQUENCE: 1
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29 qgtcaaggtt cctttcgagg ctgtctccca agccctaac tagtgacttc cactgtggcg 120
30 qgcaggggag ccattggcag aacctagcca gtcaggaaac tgcctctctt ccctcattat 180
31 cctctccctg gcattgcttt gctcgggtcc agctcagttg gtgaecgggc ccctctccc 240
32 cagggttgga tccacggaag caggggtgca ggcgggccag gcactgtgcc atgagccaga 300
33 gcccgaggtt cgtgaccggg agggggcggt ctctaaaggc tgccctgga gccggcacc 360
34 ggcgcaacga gagccaggac tatttgcctg tggacgagct gggagacgac ggcctaccgc 420
35 agctcccgct gccaccgtat ggcctactac ccagcttccg gggtaatgaa aacagactga 480
36 ctccacggcg gcagacgatt ctctgtgaga agggaagaag gttagctaat cagaggaccag 540
37 catacatgtt taatgatcat tcaacaagcc tgtctattga ggaagaacgc tttctagatg 600
38 cagttgaata tggcaacatc ccagtggtct ggaagatgct agaagagtgt cattccctca 660
39 atgttaactg tgtggattac atgggccaga atgccctaca gctggtgtg gccaatgagc 720
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41 tacttttagc cattagtaaa ggttatgtac qgatttgga gccaatctc aaccatccat 840
42 cttttgctga aggcaaaagg tttagcgaaa gccccagcca gctgaactt cagcaagatg 900
43 acttttatgc ctatgatgaa gatgggaacg ggttctccca tgatgtgact ccaatcttc 960
44 tgcctgcaca ttgccaggaa tatgaaattg tgcataccct cctgagaaag ggtgcccgga 1020
45 ttgagcggcc tcattgattac ttctgcaagt gtacagaatg cagccagaag cagaagcatg 1080
46 attccttcag ccactctaga tccaggatca atgcatacaa aggtctgga agtccagcat 1140
47 acctgtcatt gtccagtga gatccagtca tgaactgttt agaacttagc aatgagctgg 1200
48 cagtgtttgc caacattgag aaagagttca agaactgact caggaagctg tctatgcagt 1260
49 gcaaggattt cgttggttgt ctcttggaac ttgcagaaa cacagaggaa gtggaggcca 1320
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52 aacagctcct gtccatatgg tatgagaacc tctctgggtt acggcagcag accatggcag 1500
53 tgaagtctct cgtggctctt gctgttgcca ttggattgcc ctctctggt ctcatatact 1560
54 qgtgtgctcc ttgcagcaag atggggaaga tattgccag accgttcatg aagtttgtag 1620
55 cacacgcagc ctctctcacc attttctctg ggtgtctct catgaatgca gctgacagat 1680
56 ttgaaggcac caagctctc cctaataaaa ccagcacaga taatgcaagg cagctgttca 1740
57 ggatgaaaac atctgtttc tcattggttg agatgctcat tatatcttg gtaataggca 1800

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58 tgaatggaac tgaatgtaaa gaaatctgga ctcaaggccc aagaagaatc ttatttgagt 1860
59 tttggaatat gtttgacttt ggaatgctgg caatctttgc agcatcattc attgcaagat 1920
60 ttatggogtt ctggcatgca tccaaagctc agagcatcat tgatgcaaat gatactttaa 1980
61 aggatttgac aaaagtcaca ctgggggaca acgttaaata ctacaatctg gccaggataa 2040
62 agtgggaacc tactgacct cagatcattc ctgaaggctc ttatgcaatc gctgtggttt 2100
63 taagtctctc cagaatagct tacattttac cagcaaatga aagctttgga cctctgcaga 2160
64 ttctacttgg aagaacagtg aaagatatct tcaaatccat ggtcatatcc atcatggtgt 2220
65 ttgtagcctt tatgattgga atgttcaacc tttactctca ctacattggc gcaaaacaga 2280
66 atgaagcatt cacaacagtt gaggaaggtt ttaagacaat gttctgggct atctttggtc 2340
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68 aggttctgta tgggtctctat aatgtcacaa tggtcattgt tttgctaaat atgttaattg 2460
69 ctatgatcaa tagtccattc caggaaattg aggatgatgc ggaagtggag tgggaagttg 2520
70 caagggccaa attgtggttt tctactttg aggaggggag aacacttctc gtcccttcca 2580
71 atcttgtaac aagtcacaaa tcttgcttt atctctatt gaaatttaag aaatggatgt 2640
72 gtgagctcat ccagggtcaa aagcaaggct tccaagaaga tgcagagatg aacaagagaa 2700
73 atgaagaaaa gaaatttgga atttcaggaa gtcaagaaga cctttcaaaa ttttcaattg 2760
74 acaaaaatca gttggcacac acaaaacaat caagtacaag gagctcagaa gattatcatt 2820
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76 gatatgtatt gcaggcccag attgataagg agagcgatga ggtgaatgaa ggggaattga 2940
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78 actcagaaga cctagcagag ctctattaga aactcgggga gagaactgct ttagagccaa 3060
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80 ttgaagccat attattttct gacttatttt tttaagtgtc aatgataaaa agtatgttaa 3180
81 ctgataactt ggtcatttta ggtcctaact atcaagcttt ttgggagatt aaattgcatt 3240
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84 &lt;210&gt; SEQ ID NO: 2

85 &lt;211&gt; LENGTH: 930

86 &lt;212&gt; TYPE: PRT

87 &lt;213&gt; ORGANISM: Mus musculus

89 &lt;400&gt; SEQUENCE: 2

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91 1 5 10 15
92 Ala Ala Pro Gly Ala Gly Thr Arg Arg Asn Glu Ser Gln Asp Tyr Leu
93 20 25 30
94 Leu Met Asp Glu Leu Gly Asp Asp Gly Tyr Pro Gln Leu Pro Leu Pro
95 35 40 45
96 Pro Tyr Gly Tyr Tyr Pro Ser Phe Arg Gly Asn Glu Asn Arg Leu Thr
97 50 55 60
98 His Arg Arg Gln Thr Ile Leu Arg Glu Lys Gly Arg Arg Leu Ala Asn
99 65 70 75 80
100 Arg Gly Pro Ala Tyr Met Phe Asn Asp His Ser Thr Ser Leu Ser Ile
101 85 90 95
102 Glu Glu Glu Arg Phe Leu Asp Ala Val Glu Tyr Gly Asn Ile Pro Val
103 100 105 110
104 Val Trp Lys Met Leu Glu Glu Cys His Ser Leu Asn Val Asn Cys Val
105 115 120 125
106 Asp Tyr Met Gly Gln Asn Ala Leu Gln Leu Ala Val Ala Asn Glu His
107 130 135 140
108 Leu Glu Ile Thr Glu Leu Leu Leu Lys Lys Glu Asn Leu Ser Arg Val

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 109 | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |     |
| 110 | Gly | Asp | Ala | Leu | Leu | Leu | Ala | Ile | Ser | Lys | Gly | Tyr | Val | Arg | Ile | Val |
| 111 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| 112 | Glu | Ala | Ile | Leu | Asn | His | Pro | Ser | Phe | Ala | Glu | Gly | Lys | Arg | Leu | Ala |
| 113 |     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |
| 114 | Ihr | Ser | Pro | Ser | Gln | Ser | Glu | Leu | Gln | Gln | Asp | Asp | Phe | Tyr | Ala | Tyr |
| 115 |     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| 116 | Asp | Glu | Asp | Gly | Thr | Arg | Phe | Ser | His | Asp | Val | Thr | Pro | Ile | Ile | Leu |
| 117 |     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| 118 | Ala | Ala | His | Cys | Gln | Glu | Tyr | Glu | Ile | Val | His | Ihr | Leu | Leu | Arg | Lys |
| 119 | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| 120 | Gly | Ala | Arg | Ile | Glu | Arg | Pro | His | Asp | Tyr | Phe | Cys | Lys | Cys | Thr | Glu |
| 121 |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| 122 | Cys | Ser | Gln | Lys | Gln | Lys | His | Asp | Ser | Phe | Ser | His | Ser | Arg | Ser | Arg |
| 123 |     |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |
| 124 | Ile | Asn | Ala | Tyr | Lys | Gly | Leu | Ala | Ser | Pro | Ala | Tyr | Leu | Ser | Leu | Ser |
| 125 |     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| 126 | Ser | Glu | Asp | Pro | Val | Met | Thr | Ala | Leu | Glu | Leu | Ser | Asn | Glu | Leu | Ala |
| 127 |     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| 128 | Val | Leu | Ala | Asn | Ile | Glu | Lys | Glu | Phe | Lys | Asn | Asp | Tyr | Arg | Lys | Leu |
| 129 | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| 130 | Ser | Met | Gln | Cys | Lys | Asp | Phe | Val | Val | Gly | Leu | Leu | Asp | Leu | Cys | Arg |
| 131 |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| 132 | Asn | Thr | Glu | Glu | Val | Glu | Ala | Ile | Leu | Asn | Gly | Asp | Ala | Glu | Thr | Arg |
| 133 |     |     | 340 |     |     |     |     |     |     | 345 |     |     |     | 350 |     |     |
| 134 | Gln | Pro | Gly | Asp | Phe | Gly | Arg | Pro | Asn | Leu | Ser | Arg | Leu | Lys | Leu | Ala |
| 135 |     |     | 355 |     |     |     |     |     |     | 360 |     |     |     | 365 |     |     |
| 136 | Ile | Lys | Asp | Glu | Val | Lys | Lys | Phe | Val | Ala | His | Pro | Asn | Cys | Gln | Gln |
| 137 |     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |
| 138 | Gln | Leu | Leu | Ser | Ile | Trp | Tyr | Glu | Asn | Leu | Ser | Gly | Leu | Arg | Gln | Gln |
| 139 | 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     | 400 |     |
| 140 | Thr | Met | Ala | Val | Lys | Phe | Leu | Val | Val | Leu | Ala | Val | Ala | Ile | Gly | Leu |
| 141 |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| 142 | Pro | Phe | Leu | Ala | Leu | Ile | Tyr | Trp | Cys | Ala | Pro | Cys | Ser | Lys | Met | Gly |
| 143 |     |     |     | 420 |     |     |     |     |     | 425 |     |     |     | 430 |     |     |
| 144 | Lys | Ile | Leu | Pro | Arg | Pro | Phe | Met | Lys | Phe | Val | Ala | His | Ala | Ala | Ser |
| 145 |     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |
| 146 | Phe | Thr | Ile | Phe | Leu | Gly | Leu | Leu | Val | Met | Asn | Ala | Ala | Asp | Arg | Phe |
| 147 |     | 450 |     |     |     |     | 455 |     |     |     |     |     |     | 460 |     |     |
| 148 | Glu | Gly | Thr | Lys | Leu | Leu | Pro | Asn | Glu | Thr | Ser | Thr | Asp | Asn | Ala | Arg |
| 149 | 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |
| 150 | Gln | Leu | Phe | Arg | Met | Lys | Thr | Ser | Cys | Phe | Ser | Trp | Met | Glu | Met | Leu |
| 151 |     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |
| 152 | Ile | Ile | Ser | Trp | Val | Ile | Gly | Met | Ile | Trp | Ala | Glu | Cys | Lys | Glu | Ile |
| 153 |     |     | 500 |     |     |     |     |     |     | 505 |     |     |     |     | 510 |     |
| 154 | Trp | Thr | Gln | Gly | Pro | Lys | Glu | Tyr | Leu | Phe | Glu | Leu | Trp | Asn | Met | Leu |
| 155 |     |     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |
| 156 | Asp | Phe | Gly | Met | Leu | Ala | Ile | Phe | Ala | Ala | Ser | Phe | Ile | Ala | Arg | Phe |
| 157 |     | 530 |     |     |     |     | 535 |     |     |     |     |     |     | 540 |     |     |

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Input Set : A:\PIO.AMC.txt

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158 Met Ala Phe Trp His Ala Ser Lys Ala Gln Ser Ile Ile Asp Ala Asn
159 545 550 555 560
160 Asp Thr Leu Lys Asp Leu Thr Lys Val Thr Leu Gly Asp Asn Val Lys
161 565 570 575
162 Tyr Tyr Asn Leu Ala Arg Ile Lys Trp Asp Pro Thr Asp Pro Gln Ile
163 580 585 590
164 Ile Ser Glu Gly Leu Tyr Ala Ile Ala Val Val Leu Ser Phe Ser Arg
165 595 600 605
166 Ile Ala Tyr Ile Leu Pro Ala Asn Glu Ser Phe Gly Pro Leu Gln Ile
167 610 615 620
168 Ser Leu Gly Arg Thr Val Lys Asp Ile Phe Lys Phe Met Val Ile Phe
169 625 630 635 640
170 Ile Met Val Phe Val Ala Phe Met Ile Gly Met Phe Asn Leu Tyr Ser
171 645 650 655
172 Tyr Tyr Ile Gly Ala Lys Gln Asn Glu Ala Phe Thr Thr Val Glu Glu
173 660 665 670
174 Ser Phe Lys Thr Leu Phe Trp Ala Ile Phe Gly Leu Ser Glu Val Lys
175 675 680 685
176 Ser Val Val Ile Asn Tyr Asn His Lys Phe Ile Glu Asn Ile Gly Tyr
177 690 695 700
178 Val Leu Tyr Gly Val Tyr Asn Val Thr Met Val Ile Val Leu Leu Asn
179 705 710 715 720
180 Met Leu Ile Ala Met Ile Asn Ser Ser Phe Gln Glu Ile Glu Asp Asp
181 725 730 735
182 Ala Asp Val Glu Trp Lys Phe Ala Arg Ala Lys Leu Trp Phe Ser Tyr
183 740 745 750
184 Phe Glu Glu Gly Arg Thr Leu Pro Val Pro Phe Asn Leu Val Pro Ser
185 755 760 765
186 Pro Lys Ser Leu Leu Tyr Leu Leu Leu Lys Phe Lys Lys Trp Met Cys
187 770 775 780
188 Glu Leu Ile Gln Gly Gln Lys Gln Gly Phe Gln Glu Asp Ala Glu Met
189 785 790 795 800
190 Asn Lys Arg Asn Glu Lys Lys Phe Gly Ile Ser Gly Ser His Glu
191 805 810 815
192 Asp Leu Ser Lys Phe Ser Leu Asp Lys Asn Gln Leu Ala His Asn Lys
193 820 825 830
194 Gln Ser Ser Thr Arg Ser Ser Glu Asp Tyr His Leu Asn Ser Phe Ser
195 835 840 845
196 Asn Pro Pro Arg Gln Tyr Gln Lys Ile Met Lys Arg Leu Ile Lys Arg
197 850 855 860
198 Tyr Val Leu Gln Ala Gln Ile Asp Lys Glu Ser Asp Glu Val Asn Glu
199 865 870 875 880
200 Gly Glu Leu Lys Glu Ile Lys Gln Asp Ile Ser Ser Leu Arg Tyr Glu
201 885 890 895
202 Leu Leu Glu Glu Lys Ser Gln Asn Ser Glu Asp Leu Ala Glu Leu Ile
203 900 905 910
204 Arg Lys Leu Gly Glu Arg Leu Ser Leu Glu Pro Lys Leu Glu Glu Ser
205 915 920 925
206 Arg Arg

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Output Set: N:\CRF3\12312001\J005216.raw

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207      930
210 <210> SEQ ID NO: 3
211 <211> LENGTH: 200
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Targeting vector
218 <400> SEQUENCE: 3
219 tcttcaattc taactgcatt tcttctggaa aagaataaaa cgattcacca gagctccaga 60
220 gqatagccta agctgagttg tttttaatca aatcattctg tgtgctgtct cacccttagt 120
221 ttcttgcctc tccaagctgt cagcaacagc tctgtccat atggtatgag aacctctctg 180
222 gtttacggca gcagaccatg                               200
224 <210> SEQ ID NO: 4
225 <211> LENGTH: 200
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Targeting vector
232 <400> SEQUENCE: 4
233 tcttggctct tgcgtgtgcc attggattgc ccttctggc tctcatatac tgggtgtgctc 60
234 cttagcagcaa ggtatgtctg tgagtcctgc agtccatctg tagttgaatt ctgtccagca 120
235 ggcaaagatc tagctccaaa atgaaaatat gatttgaagt acacagggtc acataatctt 180
236 tctatttggt tgagaatttc                               200

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\12312001\J005216.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date